



# 9

## SEQUENCE LISTING

A/1  
<110> Kumar, Rajesh  
Sahni, Girish  
Roy, Chait  
Rajagopal, Kammara  
Nihalani, Deepak  
Sundaram, Vasudha  
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE  
PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION  
CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID  
PROTEIN

<130> 07064-009002

<140> 09/940,235  
<141> 2001-08-27

<150> 09/471,349  
<151> 1999-12-23

<150> IN 3825/DEL/98  
<151> 1998-12-24

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 1245  
<212> DNA  
<213> Streptococcus equisimilis

<220>  
<221> CDS  
<222> (1)...(1242)

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1 5 10 15

48

caa tta gtt gtt agc gtt gct act gtt gag ggg acg aat caa gac  
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp  
20 25 30

96

att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat  
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His  
35 40 45

144

gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct  
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala  
50 55 60

192

act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta		240	
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu			
65	70	75	80
aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac		288	
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp			
85	90	95	
tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga		336	
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg			
100	105	110	
aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg		384	
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro			
115	120	125	
acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga		432	
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg			
130	135	140	
cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg		480	
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val			
145	150	155	160
gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga		528	
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg			
165	170	175	
cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac		576	
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp			
180	185	190	
acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac		624	
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn			
195	200	205	
aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc		672	
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val			
210	215	220	
act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag		720	
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu			
225	230	235	240
ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa		768	
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys			
245	250	255	
aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag		816	
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu			
260	265	270	
aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat		864	
Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp			
275	280	285	

cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc		912	
Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr			
290	295	300	
aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac		960	
Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn			
305	310	315	320
tta gac ttc aga gat tta tac gat cct cgt gat aag gct aaa cta ctc		1008	
Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu			
325	330	335	
tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga		1056	
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly			
340	345	350	
aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat		1104	
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr			
355	360	365	
atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat		1152	
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr			
370	375	380	
gat aaa gat cgt tat acc gaa gaa gaa cga gaa gtt tac agc tac ctg		1200	
Asp Lys Asp Arg Tyr Thr Glu Glu Arg Glu Val Tyr Ser Tyr Leu			
385	390	395	400
cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa		1242	
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys			
405	410		
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<211> 414			
<212> PRT			
<213> Streptococcus equisimilis			
<400> 2			
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Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His			
35	40	45	
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala			
50	55	60	
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu			
65	70	75	80
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp			
85	90	95	
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg			
100	105	110	
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro			
115	120	125	
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg			

130	135	140
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val		
145	150	155
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg		
165	170	175
Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp		
180	185	190
Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ser Ile Leu Asn		
195	200	205
Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val		
210	215	220
Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu		
225	230	235
Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys		
245	250	255
Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu		
260	265	270
Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp		
275	280	285
Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr		
290	295	300
Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn		
305	310	315
Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu		
325	330	335
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly		
340	345	350
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr		
355	360	365
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr		
370	375	380
Asp Lys Asp Arg Tyr Thr Glu Glu Glu Arg Glu Val Tyr Ser Tyr Leu		
385	390	395
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys		
405	410	

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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)...(777)

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Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser Gln  
1 5 10 15

48  
agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa  
Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln  
20 25 30

96  
cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat  
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr  
35 40 45

144

gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu	192
50 55 60	
act tgc ttt gac aag tac act ggg aac act tac cga gtg ggt gac act Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr	240
65 70 75 80	
tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly	288
85 90 95	
gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu	336
100 105 110	
ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu	384
115 120 125	
act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly	432
130 135 140	
gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala	480
145 150 155 160	
ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly	528
165 170 175	
tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile	576
180 185 190	
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser	624
195 200 205	
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu	672
210 215 220	
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu	720
225 230 235 240	
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc Arg His Thr Ser Val Gln Thr Ser Ser Gly Ser Gly Pro Phe Thr	768
245 250 255	
gat gtt cgt Asp Val Arg	777

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<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 4  
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Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln  
20 25 30  
Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr  
35 40 45  
Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu  
50 55 60  
Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr  
65 70 75 80  
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly  
85 90 95  
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu  
100 105 110  
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu  
115 120 125  
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly  
130 135 140  
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala  
145 150 155 160  
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly  
165 170 175  
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile  
180 185 190  
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser  
195 200 205  
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu  
210 215 220  
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu  
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Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr  
245 250 255  
Asp Val Arg

<210> 5  
<211> 1377  
<212> DNA  
<213> Streptococcus equisimilis

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ctaagcggac atgtgcgcgt tagaccatat aaagaaaaac caatacaaaa ccaagcgaaa	600
tctgttcatg tggaatatac tgtacagttt actcccttaa accctgatga cgatttcaga	660
ccagggtctca aagataactaa gctattgaaa acactagcta tcggtgacac catcacatct	720
caagaattac tagctcaagc acaaaggcatt ttaaacaaaa accacccagg ctatacgatt	780
tatgaacgtq actcctcaat cgtcactcat gacaatgaca tttccgtac gattttacca	840
atggatcaag agtttactta ccgtgttaaa aatcgggAAC aagcttatacg gatcaataaa	900
aaatctggtc tgaatgaaga aataaacaac actgacctga tctctgagaa atattacgtc	960
cttaaaaaag gggAAAAGCC gtatgatccc ttgatcgca gtcacttggaa actgttcacc	1020
atcaaatacg ttgatgtcga taccaacgaa ttgctaaaaa gtgagcagct cttacagct	1080
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aatcagcatg acaccaaccc tatcataacc gtttatatgg gcaagcgacc cgaaggagag	1260
aatgctagct atcatttagc ctatgataaa gatcggtata ccgaagaaga acgagaagtt	1320
tacagctacc tgcggttatac agggacaccc tacatgtata accctaacga caaataaa	1377

&lt;210&gt; 6

&lt;211&gt; 1327

&lt;212&gt; DNA

&lt;213&gt; Streptococcus equisimilis

&lt;400&gt; 6

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catcacatct caagaattac tagctcaagc acaaaggcatt ttaaacaaaa accacccagg	720
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cgaaggagag aatgctagct atcatttagc ctatgataaa gatcggtata ccgaagaaga	1260
acgagaagtt tacagctacc tgcggttatac agggacaccc tacatgtata accctaacga	1320
caaataaa	1377

&lt;210&gt; 7

&lt;211&gt; 52

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Chimeric gene

&lt;221&gt; CDS

&lt;222&gt; (2)...(49)

&lt;400&gt; 7

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ccc . . . 52

<210> 8  
<211> 16  
<212> PRT  
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<220>  
<223> Chimeric peptide

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1 5 10 15

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<212> DNA  
<213> Artificial Sequence
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<220>  
<223> Hybrid cassette

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atcaagacat	tagtcttaaa	tttttgaaa	tcgatctaac	atcacgacct	gctcatggag	180
gaaagacaga	gcaaggctta	agtccaaaat	caaaaccatt	tgctactgtat	agtggcgacg	240
tgtcacataa	acttgagaaa	gctgacttac	taaaggctat	tcaagaacaa	ttgatcgcta	300
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tcggtgacac	catcacatct	caagaattac	tagctcaagc	acaaagcattt	ttaaacaaaa	660
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taactggaaa	agtagaggat	aatcacgatg	acaccaaccg	tatcataacc	gttttatatgg	1140
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gagaaacgtg	ggagaagccc	taccaaggct	ggatgatgg	agattgtact	tcgcggag	1320
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catcctatag	aattggagac	acctggagca	agaaggataa	tgcaggaaac	ctgctccagt	1440
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<210> 10  
<211> 1661  
<212> DNA

<213> Artificial Sequence

<220>

<223> Hybrid cassette

<400> 10

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agaccacaac	ggttccctc	tagaaataat	tttgttaac	ttaagaagg	agatatacca	180
tgattgctgg	acctgagtgg	ctgctagacc	gtccatctgt	caacaacagc	caattgggt	240
tttagcgttgc	tggtactgtt	gaggggacga	atcaagacat	tagtcttaaa	tttttgaaa	300
tcgatctaac	atcacgacct	gctcatggag	gaaagacaga	gcaaggctta	agtccaaaat	360
caaaaccatt	tgctactgat	agtggcgcga	tgtcacataa	acttgagaaa	gctgacttac	420
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atgtgcgcgt	tagaccatat	aaagaaaaac	caatacaaaa	ccaagcggaaa	tctgttgatg	660
tggaatatac	tgtacagttt	actcccttaa	accctgtatga	cgatttcaga	ccaggtctca	720
aagatactaa	gctattgaaa	acactagcta	tcggtgacac	catcacatct	caagaattac	780
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43

SEQUENCE LISTING

<110> Sahni, Girish  
Kumar, Rajesh  
Roy, Chaiti  
Rajagopal, Kammara  
Nihalani, Deepak  
Sundaram, Vasudha  
Yadav, Mahavir

<120> NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID PROTEINS

<130> 07064/009001

<140> US 09/471,349  
<141> 1999-12-23

<150> IN 3825/DEL/98  
<151> 1998-12-24

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1 5 10 15		
caa tta gtt gtt agc gtt gct ggt act gtt gag ggg acg aat caa gac		96
Gln Leu Val Val Ser Val Ala Gly Thr Val Glu Gly Thr Asn Gln Asp		
20 25 30		
att agt ctt aaa ttt ttt gaa atc gat cta aca tca cga cct gct cat		144
Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His		
35 40 45		
gga gga aag aca gag caa ggc tta agt cca aaa tca aaa cca ttt gct		192
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala		
50 55 60		
act gat agt ggc gcg atg tca cat aaa ctt gag aaa gct gac tta cta		240
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu		
65 70 75 80		

aag gct att caa gaa caa ttg atc gct aac gtc cac agt aac gac gac Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp	85	90	95	288
tac ttt gag gtc att gat ttt gca agc gat gca acc att act gat cga Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg	100	105	110	336
aac ggc aag gtc tac ttt gct gac aaa gat ggt tcg gta acc ttg ccg Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro	115	120	125	384
acc caa cct gtc caa gaa ttt ttg cta agc gga cat gtg cgc gtt aga Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg	130	135	140	432
cca tat aaa gaa aaa cca ata caa aac caa gcg aaa tct gtt gat gtg Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val	145	150	155	480
160				
gaa tat act gta cag ttt act ccc tta aac cct gat gac gat ttc aga Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Phe Arg	165	170	175	528
cca ggt ctc aaa gat act aag cta ttg aaa aca cta gct atc ggt gac Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp	180	185	190	576
195				
acc atc aca tct caa gaa tta cta gct caa gca caa agc att tta aac Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn	200	205		624
210				
aaa aac cac cca ggc tat acg att tat gaa cgt gac tcc tca atc gtc Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val	215	220		672
225				
act cat gac aat gac att ttc cgt acg att tta cca atg gat caa gag Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu	230	235	240	720
245				
ttt act tac cgt gtt aaa aat cgg gaa caa gct tat agg atc aat aaa Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys	250	255		768
260				
aaa tct ggt ctg aat gaa gaa ata aac aac act gac ctg atc tct gag Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu	265	270		816
275				
aaa tat tac gtc ctt aaa aaa ggg gaa aag ccg tat gat ccc ttt gat Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp	280	285		864
290				
cgc agt cac ttg aaa ctg ttc acc atc aaa tac gtt gat gtc gat acc Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr	295	300		912
300				
aac gaa ttg cta aaa agt gag cag ctc tta aca gct agc gaa cgt aac				960

Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn				
305	310	315	320	
tta gac ttc aga gat tta tac gat cct cgt gat aag gct aaa cta ctc				1008
Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu				
325	330	335		
tac aac aat ctc gat gct ttt ggt att atg gac tat acc tta act gga				1056
Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly				
340	345	350		
aaa gta gag gat aat cac gat gac acc aac cgt atc ata acc gtt tat				1104
Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr				
355	360	365		
atg ggc aag cga ccc gaa gga gag aat gct agc tat cat tta gcc tat				1152
Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr				
370	375	380		
gat aaa gat cgt tat acc gaa gaa cga gaa gtt tac agc tac ctg				1200
Asp Lys Asp Arg Tyr Thr Glu Glu Arg Glu Val Tyr Ser Tyr Leu				
385	390	395	400	
cgt tat aca ggg aca cct ata cct gat aac cct aac gac aaa				1242
Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys				
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taa				1245

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<212> PRT  
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Ile Ser Leu Lys Phe Phe Glu Ile Asp Leu Thr Ser Arg Pro Ala His				
35	40	45		
Gly Gly Lys Thr Glu Gln Gly Leu Ser Pro Lys Ser Lys Pro Phe Ala				
50	55	60		
Thr Asp Ser Gly Ala Met Ser His Lys Leu Glu Lys Ala Asp Leu Leu				
65	70	75	80	
Lys Ala Ile Gln Glu Gln Leu Ile Ala Asn Val His Ser Asn Asp Asp				
85	90	95		
Tyr Phe Glu Val Ile Asp Phe Ala Ser Asp Ala Thr Ile Thr Asp Arg				
100	105	110		
Asn Gly Lys Val Tyr Phe Ala Asp Lys Asp Gly Ser Val Thr Leu Pro				
115	120	125		
Thr Gln Pro Val Gln Glu Phe Leu Leu Ser Gly His Val Arg Val Arg				
130	135	140		
Pro Tyr Lys Glu Lys Pro Ile Gln Asn Gln Ala Lys Ser Val Asp Val				
145	150	155	160	
Glu Tyr Thr Val Gln Phe Thr Pro Leu Asn Pro Asp Asp Asp Phe Arg				
165	170	175		

Pro Gly Leu Lys Asp Thr Lys Leu Leu Lys Thr Leu Ala Ile Gly Asp  
     180                     185                     190  
 Thr Ile Thr Ser Gln Glu Leu Leu Ala Gln Ala Gln Ser Ile Leu Asn  
     195                     200                     205  
 Lys Asn His Pro Gly Tyr Thr Ile Tyr Glu Arg Asp Ser Ser Ile Val  
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 Thr His Asp Asn Asp Ile Phe Arg Thr Ile Leu Pro Met Asp Gln Glu  
     225                     230                     235                     240  
 Phe Thr Tyr Arg Val Lys Asn Arg Glu Gln Ala Tyr Arg Ile Asn Lys  
     245                     250                     255  
 Lys Ser Gly Leu Asn Glu Glu Ile Asn Asn Thr Asp Leu Ile Ser Glu  
     260                     265                     270  
 Lys Tyr Tyr Val Leu Lys Lys Gly Glu Lys Pro Tyr Asp Pro Phe Asp  
     275                     280                     285  
 Arg Ser His Leu Lys Leu Phe Thr Ile Lys Tyr Val Asp Val Asp Thr  
     290                     295                     300  
 Asn Glu Leu Leu Lys Ser Glu Gln Leu Leu Thr Ala Ser Glu Arg Asn  
     305                     310                     315                     320  
 Leu Asp Phe Arg Asp Leu Tyr Asp Pro Arg Asp Lys Ala Lys Leu Leu  
     325                     330                     335  
 Tyr Asn Asn Leu Asp Ala Phe Gly Ile Met Asp Tyr Thr Leu Thr Gly  
     340                     345                     350  
 Lys Val Glu Asp Asn His Asp Asp Thr Asn Arg Ile Ile Thr Val Tyr  
     355                     360                     365  
 Met Gly Lys Arg Pro Glu Gly Glu Asn Ala Ser Tyr His Leu Ala Tyr  
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 Asp Lys Asp Arg Tyr Thr Glu Glu Arg Glu Val Tyr Ser Tyr Leu  
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 Arg Tyr Thr Gly Thr Pro Ile Pro Asp Asn Pro Asn Asp Lys  
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 agc aag ccc ggt tgt tat gac aat gga aaa cac tat cag ata aat caa     96  
 Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn Gln  
     20                     25                     30  
  
 cag tgg gag cgg acc tac cta ggt aat gtg ttg gtt tgt act tgt tat     144  
 Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys Tyr  
     35                     40                     45  
  
 gga gga agc cga ggt ttt aac tgc gaa agt aaa cct gaa gct gaa gag     192  
 Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu Glu  
     50                     55                     60

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Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr	
65 70 75 80	
tat gag cgt cct aaa gac tcc atg atc tgg gac tgt acc tgc atc ggg	288
Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly	
85 90 95	
gct ggg cga ggg aga ata agc tgt acc atc gca aac cgc tgc cat gaa	336
Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu	
100 105 110	
ggg ggt cag tcc tac aag att ggt gac acc tgg agg aga cca cat gag	384
Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu	
115 120 125	
act ggt ggt tac atg tta gag tgt gtg tgt ctt ggt aat gga aaa gga	432
Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly	
130 135 140	
gaa tgg acc tgc aag ccc ata gct gag aag tgt ttt gat cat gct gct	480
Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala	
145 150 155 160	
ggg act tcc tat gtg gtc gga gaa acg tgg gag aag ccc tac caa ggc	528
Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly	
165 170 175	
tgg atg atg gta gat tgt act tgc ctg gga gaa ggc agc gga cgc atc	576
Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg Ile	
180 185 190	
act tgc act tct aga aat aga tgc aac gat cag gac aca agg aca tcc	624
Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr Ser	
195 200 205	
tat aga att gga gac acc tgg agc aag aag gat aat cga gga aac ctg	672
Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn Leu	
210 215 220	
ctc cag tgc atc tgc aca ggc aac ggc cga gga gag tgg aag tgt gag	720
Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys Glu	
225 230 235 240	
agg cac acc tct gtg cag acc aca tcg agc gga tct ggc ccc ttc acc	768
Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe Thr	
245 250 255	
gat gtt cgt	777
Asp Val Arg	

<210> 4  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 4

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				20				25						30	
Gln	Trp	Glu	Arg	Thr	Tyr	Leu	Gly	Asn	Val	Leu	Val	Cys	Thr	Cys	Tyr
				35			40					45			
Gly	Gly	Ser	Arg	Gly	Phe	Asn	Cys	Glu	Ser	Lys	Pro	Glu	Ala	Glu	Glu
				50			55				60				
Thr	Cys	Phe	Asp	Lys	Tyr	Thr	Gly	Asn	Thr	Tyr	Arg	Val	Gly	Asp	Thr
				65			70			75			80		
Tyr	Glu	Arg	Pro	Lys	Asp	Ser	Met	Ile	Trp	Asp	Cys	Thr	Cys	Ile	Gly
				85				90					95		
Ala	Gly	Arg	Gly	Arg	Ile	Ser	Cys	Thr	Ile	Ala	Asn	Arg	Cys	His	Glu
				100				105				110			
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Thr	Gly	Gly	Tyr	Met	Leu	Glu	Cys	Val	Cys	Leu	Gly	Asn	Gly	Lys	Gly
				130			135				140				
Glu	Trp	Thr	Cys	Lys	Pro	Ile	Ala	Glu	Lys	Cys	Phe	Asp	His	Ala	Ala
				145			150			155			160		
Gly	Thr	Ser	Tyr	Val	Val	Gly	Glu	Thr	Trp	Glu	Lys	Pro	Tyr	Gln	Gly
				165				170				175			
Trp	Met	Met	Val	Asp	Cys	Thr	Cys	Leu	Gly	Glu	Gly	Ser	Gly	Arg	Ile
				180				185				190			
Thr	Cys	Thr	Ser	Arg	Asn	Arg	Cys	Asn	Asp	Gln	Asp	Thr	Arg	Thr	Ser
				195				200			205				
Tyr	Arg	Ile	Gly	Asp	Thr	Trp	Ser	Lys	Lys	Asp	Asn	Arg	Gly	Asn	Leu
				210			215			220					
Leu	Gln	Cys	Ile	Cys	Thr	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Lys	Cys	Glu
				225			230			235			240		
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Asp	Val	Arg													

<210> 5  
<211> 1377  
<212> DNA  
<213> Streptococcus equisimilis

<400> 5

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agatatacca	tgattgctgg	acctgagtg	ctgctagacc	gtccatctgt	caacaacagc	180
caattggttg	ttagcgttgc	tgtactgtt	gagggacgca	atcaagacat	tagcttaaa	240
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caagaattac	tagctcaagc	acaaagcatt	ttaaacaaaaa	accaccccagg	ctatacgatt	780
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aatcacgatg acaccaaccg tatkataacc gtttatatgg gcaagcgacc cgaaggagag	1260
aatgctagct atcatttgc ctatgataaa gatcggtata ccgaagaaga acgagaagtt	1320
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<210> 6  
<211> 1327  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetically generated primer

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aaataacagc caattgttg ttacgttgc tggactgtt gaggggacga atcaagacat	180
tagtctaaa tttttgaaa tcgatctaac atcacgacct gctcatggag gaaagacaga	240
gcaaggctt agtccaaaat caaaaccatt tgctactgat agtggcgcga tgtcacataa	300
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taacgacgac tactttgagg tcattgattt tgcaagcgat gcaaccatta ctgatcgaaa	420
cggcaagggtc tactttgctg acaaagatgg ttcggtaacc ttgccgaccc aacctgtcca	480
agaatttttgc ttaagcgac atgtgcgcgt tagaccatat aaagaaaaac caataaaaaa	540
ccaagcgaaa tctgttgc tgaatatac tgtacagttt actcccttaa accctgatga	600
cgatttcaga ccaggctca aagatactaa gctattgaaa acactagcta tcggtgacac	660
catcacatct caagaattac tagctcaagc acaaagcatt ttaaacaaaa accacccagg	720
ctatacgatt tatgaacgtg actcctcaat cgtaactcat gacaatgaca tttccgtac	780
gattttacca atggatcaag agtttactta ccgtttaaa aatcggaac aagcttata	840
gatcaataaaa aaatctggtc tgaatgaaga aataaacaac actgacctga tctctgagaa	900
atattacgtc cttaaaaaaa gggaaaagcc gtatgatccc tttgatcgca gtcactgaa	960
actgttcacc atcaaatacg ttgatgtcga taccaacgaa ttgctaaaaa gtgagcagct	1020
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taaactactc tacaacaatc tcgatgttt tggattatg gactatacct taactggaaa	1140
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cgaaggagag aatgctagct atcatttgc ctatgataaa gatcggtata ccgaagaaga	1260
acgagaagtt tacagctacc tgcgttatac agggacacct atacctgata accctaacga	1320
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<210> 7  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetically generated primer

<221> CDS  
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1 5 10 15	

ccc  
Pro

52

<210> 8  
<211> 17  
<212> PRT  
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<220>  
<223> Synthetically generated protein

<400> 8  
Asn Ala Ser Tyr His Leu Ala Gly Gly Gln Ala Gln Gln Ile Val  
1 5 10 15  
Pro

<210> 9  
<211> 1541  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetically generated primer

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atcaagacat tagtctaaa tttttgaaa tcgatctaacc atcacgaccc gctcatggag 180  
gaaagacaga gcaaggctt agtccaaaat caaaaccatt tgctactgtt agtggcgca 240  
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aacctgtcca agaatttttgc ttaagcggac atgtgcgcgt tagaccatat aaagaaaaac 480  
caatacaaaa ccaagcgaaa tctgttgcgt tggaatatac tgtacagttt actcccttaa 540  
accctgtatca cgatttcaga ccaggtctca aagataactaa gctattgaaa acactagcta 600  
tcggtgacac catcacatct caagaattac tagctcaagc acaaaagcatt ttaaaca 660  
accaccagg ctatacgatt tatgaacgtt actccctcaat cgtcactcat gacaatgaca 720  
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<210> 10  
<211> 1661

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 10

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agaccacaac ggttccctc tagaaataat ttgtttaac ttaagaagg agatatacca	180
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ttagcgttgc tggtaactgtt gaggggacga atcaagacat tagtctaaa tttttgaaa	300
tcgatctaac atcacgacct gctcatggag gaaagacaga gcaaggctt agtccaaat	360
caaaaccatt tgctactgat atggcgcgta tgtcacataa acttgagaaa gctgacttac	420
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acaaagatgg ttcggttaacc ttgccgaccc aacctgtcca agaattttt ctaagcggac	600
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tggaaataac tgcgtttt accctgtatga cgatttcaga ccaggctca	720
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<210> 11

<211> 1782

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 11

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acgctccccg agatctcgat cccgcgaat taatacgact cactataggg agaccacaac	180
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<210> 12

<211> 2096

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 12

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gtacttgcct gggagaaggc agcggacgca tcacttgcac ttcttagaaat agatgcaacg	1920
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gaaacctgct ccagtgcata tcgacaggca acggccgagg agagtggaaag tgtgagaggc	2040
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